AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph beginning on page 25, line 1, as follows:

DNA fragments containing nuclear microsatellite sequences were PCR-amplified from loblolly pine genomic DNA using 3 pairs of DNA primers. The DNA sequences for two primer pairs, PtTX3011 and PtTX3034, were obtained from the Texas A&M University web page of Dr. Claire Williams (http://forestry.tamu.edu/genetics/primer.txt). The other primer pair was designed from the loblolly pine EST sequence 6c12f (GenBank accession AA556811; see Table 2). This EST was found by conducting a BLAST search of EST sequences in GenBank using 10 repeats of the trinucleotide CAG. DNA sequence from the M13–29 forward sequencing primer was incorporated at the 5' end of each forward primer sequence (5'-CACGACGTTGTAAAACGAC-3' [SEQ ID No. 21], using the tailed primer strategy described by Oetting et al. (Genomics 30:450-458 (1995)~~; see also http://biosupport.licor.com/support/RnP/protocols/TailPrim.shtml~~). An M13 primer with a 5' infrared fluorophore label, IRD41, was used as the only source of labeled primer for detection for all nuclear microsatellites. The PCR-reactions were carried out in 10 µl using 40 ng of loblolly pine genomic DNA as template. The PCR reactions contained PCR buffer and 1 unit of Taq polymerase (Boehringer Mannheim, 10 mM Tris-HCl, 1.5 mM MgCl2, 50 mM KCl, pH 8.3), 2 pmol anti-sense primer, 0.1 pmol IR-labeled sense primer, 0.1 mM dNTP (using dGTP). The reactions were run in 96-well polycarbonate microtitre plates (25 µL conical-bottom wells). The thermocycler temperature program was [94° C, 10 s; 65° C, 30 s; 72° C, 1 m] repeated 13 times, dropping the annealing temperature by 0.7 degree each cycle, followed by 23 cycles using the [94° C, 10 s; 56° C, 30 s; 72° C]. The stop solution contained 95% formamide, 0.1 mM EDTA, 0.1% bromophenol blue, and 5 µL of stop solution was added to each reaction.

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